Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (Currently amended) A method for identifying a polynucleotide sequence, wherein the polynucleotide sequence ~~may be~~ is or is suspected of being associated with a commercially or aesthetically relevant trait, comprising:

a) aligning homologous nucleotide sequences of at least two individual organisms, wherein said at least two individual organisms are selected from the group consisting of individual organisms of a single strain, individual organisms of different strains, individual organisms of the same species, individual organisms of different species, and any combination of the foregoing, wherein one nucleotide sequence is associated with an individual organism exhibiting said commercially or aesthetically relevant trait;

b) conducting an evolutionary bottleneck analysis selected from the group consisting of assessing the number of nucleotide differences per site, assessing fraction of nucleotides shared between homologous sequences, and the silent site nucleotide diversity on the aligned homologous nucleotide sequences; and

~~b)~~ c) detecting a region of polynucleotide sequence wherein the evolutionary bottleneck analysis ~~for which the number of nucleotide differences/site~~ indicates an evolutionary bottleneck; whereby a polynucleotide sequence which is or is suspected to be associated with a commercially or aesthetically relevant trait of said organism ~~may be~~ is identified.

2. (cancelled)

3. (Currently amended) A method for identifying a polynucleotide sequence encoding a polypeptide, wherein the polypeptide ~~may be~~ is or is suspected of being associated with a commercially or aesthetically relevant trait comprising:

a) aligning homologous protein-coding nucleotide sequences of at least two individual organisms, wherein said at least two individual organisms are selected from the group consisting of individual organisms of a single strain, individual organisms of different strains,

individual organisms of the same species, individual organisms of different species, and any combination of the foregoing, wherein one nucleotide sequence encodes a polypeptide associated with ~~an~~ a domesticated organism exhibiting said commercially or aesthetically relevant trait; and

b) conducting an evolutionary bottleneck analysis selected from the group consisting of assessing the number of nucleotide differences per site, assessing fraction of nucleotides shared between homologous sequences, and the silent site nucleotide diversity on the aligned homologous nucleotide sequences; and

~~b)~~ c) detecting a region of polynucleotide sequence wherein the evolutionary bottleneck analysis ~~for which the number of nucleotide differences/site~~ indicates an evolutionary bottleneck; whereby a polynucleotide sequence which is or is suspected to be associated with a commercially or aesthetically relevant trait of said organism ~~may be~~ is identified.

4. (cancelled)

5. (Currently amended) The method of claim 1, further comprising

~~c)~~ d) determining that the region identified ~~in b)~~ c) is a non-coding region, wherein the polynucleotide sequence is a regulatory element.

6. (Previously presented) The method according to claim 1, wherein the identifying the number of nucleotide differences/site is calculated by $\pi = 1/[n(n-1)/2] \sum_{i<j} \Pi ij / L$, n is number of sequences, where i and j represent any two sequences being compared in a series of sequences and L = sequence length.

7. (Previously presented) The method according to claim 1, further comprising determining if the region displays a signature of positive selection.

8. (Previously presented) The method of Claim 7, wherein said determining comprises calculating a Ka/Ks value.

9. (Previously presented) The method according to claim 1, wherein the method is performed in an automated pipeline.

10. (Previously presented) The method according to claim 1, wherein the at least two strains and/or individuals of a single strain is at least ten strains and/or individuals of a single strain.

11. (Previously presented) The method of Claim 10, wherein the at least two strains and/or individuals of a single strain is at least fifteen strains and/or individuals of a single strain.

12. (Currently amended) A method for identifying an agent which may modulate a commercially or aesthetically relevant trait that is unique, enhanced or altered in the domesticated organism as compared to other domesticated or ancestral species of the domesticated organism, said method comprising:

(a) contacting at least one candidate agent with a cell, model system or transgenic plant or animal that expresses a polynucleotide sequence that is an evolutionary bottleneck, the polynucleotide sequence identified by an analysis selected from the group consisting of assessing the number of nucleotide differences per site, assessing fraction of nucleotides shared between homologous sequences, and the silent site nucleotide diversity; and

(b) assaying for a modulated function of the polynucleotide sequence, wherein the agent is identified by its ability to modulate function of the polypeptide encoded by the polynucleotide.

13. (Currently amended) ~~A method for correlating a nucleotide sequence which is an evolutionary bottleneck to a commercially or aesthetically relevant trait that is unique, enhanced or altered in a domesticated organism, comprising:~~

~~a) identifying a nucleotide sequence which is an evolutionary bottleneck; and~~ The method of claim 1, further comprising ~~b)~~ analyzing the functional effect of the presence or absence of the ~~identified~~ sequence identified in step (c) in ~~the~~ a domesticated organism or in a model system.

14. (Previously presented) The method of claim 1, wherein the polynucleotide sequence is a regulatory element.

15. (Previously presented) The method according to claim 3, wherein the identifying the number of nucleotide differences/site is calculated by $\pi = 1/[n(n-1)/2] \sum_{i<j} \Pi ij / L$, n is number of sequences, where i and j represent any two sequences being compared in a series of sequences and L = sequence length.

16. (Previously presented) The method according to claim 3, further comprising determining if the region displays a signature of positive selection.

17. (Previously presented) The method of Claim 16, wherein said determining comprises calculating a Ka/Ks value.

18. (Previously presented) The method according to claim 3, wherein the method is performed in an automated pipeline.

19. (Previously presented) The method according to claim 3, wherein the at least two strains and/or individuals of a single strain is at least ten strains and/or individuals of a single strain.

20. (Previously presented) The method of claim 3, wherein the at least two strains and/or individuals of a single strain is at least fifteen strains and/or individuals of a single strain.